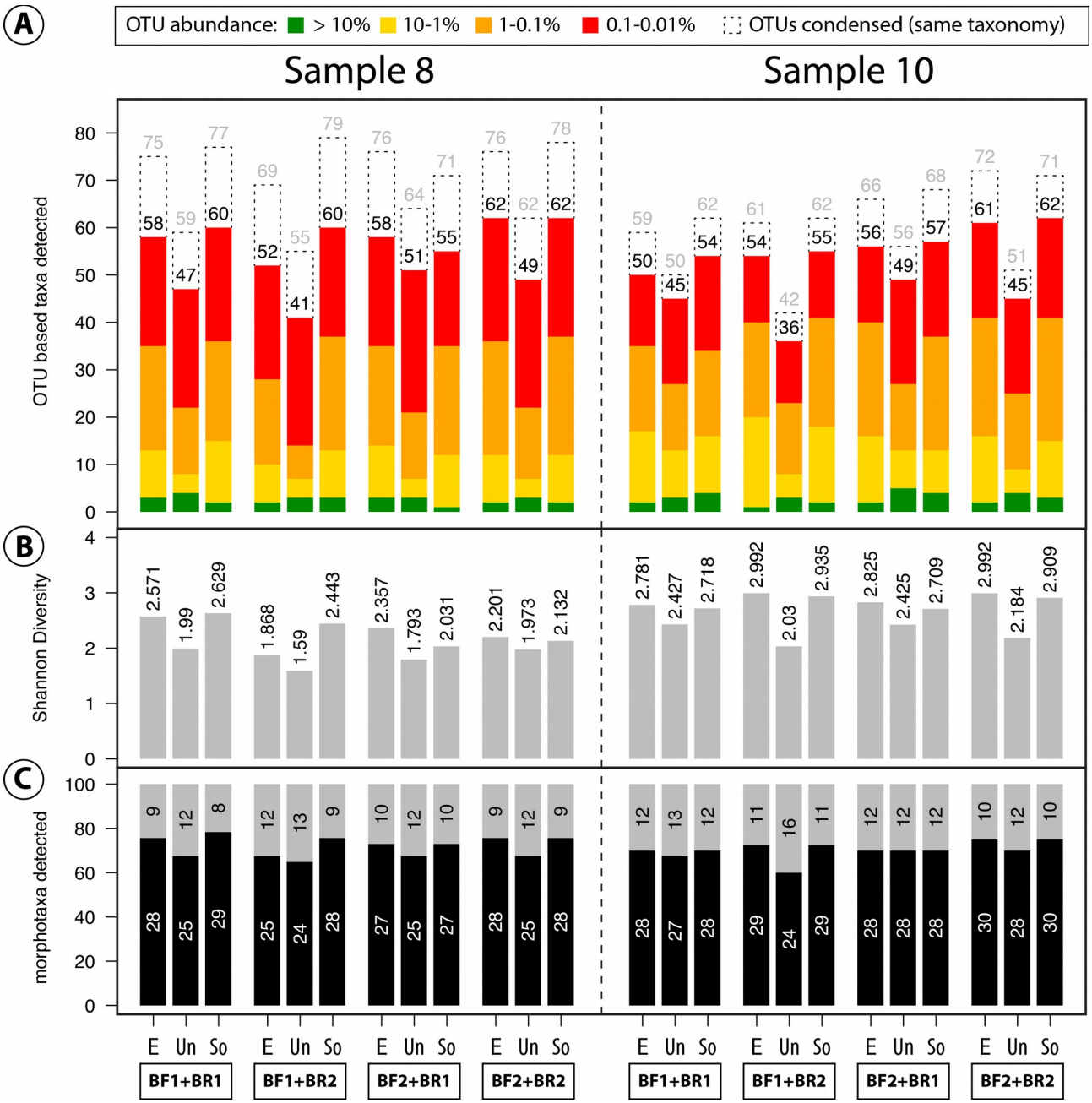

Figure S10: Comparison of taxa detection between unsorted (Un) and sorted (So) samples. Expected (E) taxa recovery was estimated by combining OTU abundances from S, M and L proportionately. **A)** Amount of OTUs and number of unique taxa identified with OTUs. OTU abundance for each taxon is indicated by color. **B)** Shannon Diversity for each sample. **C)** Proportion of morphologically identified taxa also detected with DNA metabarcoding is indicated by black bars.